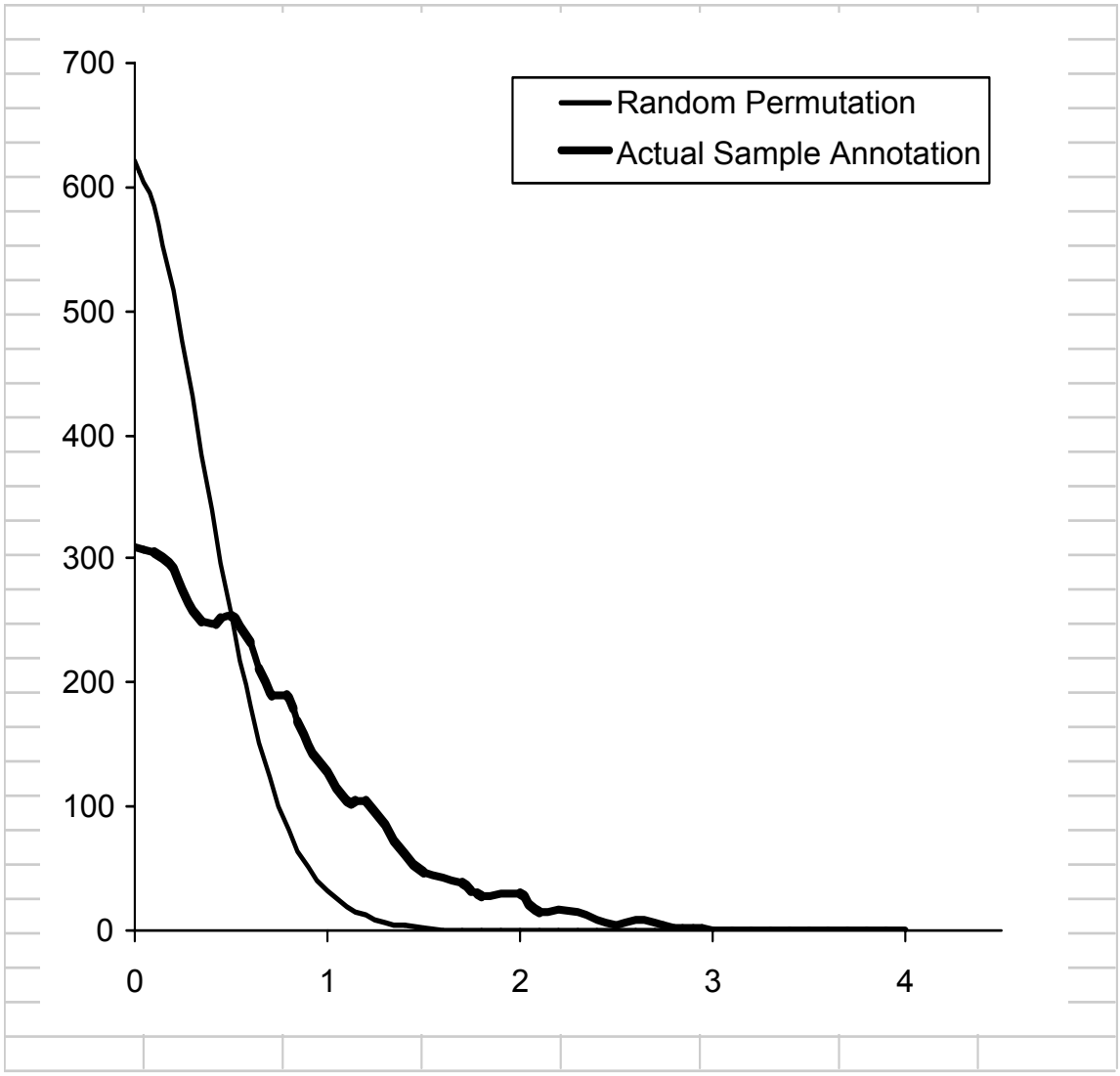
Random Permutation Test for the Significance of Discriminative Weights

In order to assess the significance of the discriminative weight that was assigned to each gene based on its ability to differentiate the two tissue types, we performed a random permutation test. We first randomly permutated the tumor type annotation for each sample in the study, then calculated discriminative weights, w, for all genes. A total of 1,000 random permutations were performed from which 3,215,000 discriminative weights were evaluated. Figure 1 shows the empirical distribution of weights obtained from original annotation of the samples (thick line), and the distribution of weights obtained from random permutations (thin line). Tabulated results from the random permutation are listed in Table 1, where the actual count for weights within each bin, and the corresponding expected random outcome, based on the random permutations, are given in columns 2 and 3, respectively. The p-value, which is defined as the probability of the discriminative weight less than or within the corresponding bin due to the pure random chance, was estimated over 1,000 permutations and provided in column 4 as a reference of significance. For example, there are a total of 210 genes with p-values less than or equal to 0.001.


700
600
500
400
300
200
100
0
0
1
2
3
4
Random Permutation
Actual Sample Annotation
Figure 1.

Bin	*Actual*	*Random*	*p-Value*
0.0 - 0.1	309	620	1
0.1 - 0.2	306	584	0.811
0.2 - 0.3	293	517	0.632
0.3 - 0.4	259	432	0.474
0.4 - 0.5	248	340	0.342
0.5 - 0.6	254	256	0.238
0.6 - 0.7	233	182	0.160
0.7 - 0.8	192	124	0.105
0.8 - 0.9	187	81	0.067
0.9 - 1.0	150	52	0.042
1.0 - 1.1	127	32	0.026
1.1 - 1.2	105	20	0.016
1.2 - 1.3	105	12	0.010
1.3 - 1.4	86	7	0.006
1.4 - 1.5	61	4	0.004
1.5 - 1.6	47	2	0.002
1.6 - 1.7	43	1	0.001
1.7 - 1.8	39	0	9.0×10^{-4}
1.8 - 1.9	27	0	6.0×10^{-4}
1.9 - 2.0	30	0	3.9×10^{-4}
2.0 - 2.1	29	0	2.6×10^{-4}
2.1 - 2.2	15	0	1.8×10^{-4}
2.2 - 2.3	18	0	1.2×10^{-4}
2.3 - 2.4	14	0	8.5×10^{-5}
2.4 - 2.5	8	0	5.8×10^{-5}
2.5 - 2.6	5	0	4.2×10^{-5}
2.6 - 2.7	8	0	3.1×10^{-5}
2.7 - 2.8	6	0	2.1×10^{-5}
2.8 - 2.9	3	0	1.6×10^{-5}
2.9 - 3.0	2	0	1.1×10^{-5}
3.0 - 3.1	1	0	8.8×10^{-6}
3.1 - 3.2	1	0	5.2×10^{-6}
3.2 - 3.3	1	0	4.0×10^{-6}
3.3 - 3.4	0	0	3.4×10^{-6}
3.4 - 3.5	1	0	2.7×10^{-6}
3.5 - 3.6	0	0	2.4×10^{-6}
3.6 - 3.7	1	0	1.5×10^{-6}
3.7 - 3.8	0	0	1.2×10^{-6}
3.8 - 3.9	0	0	1.2×10^{-6}
3.9 - 4.0	0	0	1.2×10^{-6}
> 4.0	1	0	1.2×10^{-6}

Table 1.